



# Human Immunodeficiency Virus (HIV) reverse-transcriptase region (pol gene) amplification & sequencing.

Created: Oct 26, 2010; Last modified: Mar 24, 2021, Version: 2.0

This protocol describes the nested RT-PCR approach to reverse transcriptase region (pol gene) amplification and sequencing using integrated proviral DNA or viral RNA as template. This protocol was created to allow for the characterisation of anti-retroviral drug resistance-mutations. The nested strategy allows for better success at sequencing from samples having either low quality, concentration of template or viral load (in the case of RT-PCR). The fragment thus generated partially overlaps on the 5' end with the 3' end of the protease (Prot) encoding fragment, allowing together with that of the integrase encoding fragment for the assembly of full-pol region contigs.

### **Oligonucleotides**

Name		PCR	Sequence*	bp	%GC	Tm	Position †	Amplicon	Ref.
	RT-FO2	1 <sup>st</sup> RTa	5'-ggA-AAC-CAA-AAA-TgA-TAg-gRg-gAA-3'	24	39.6	54.4	2377-2400	1.41.6	
RT-a	RT-RO3	1 KIa	5´-TCC-CAY-TCA-ggA-ATC-CAg-gT-3´	20	52.5	56.7	3774-3793	1416	
	RT-FI2	2 <sup>nd</sup> RTa	5'-Agg-TAC-AgT-ATT-AgT-Agg-ACC-TAC-3'	24	41.7	52.4	2468-2491	1050	
	RT-RI3	2 Kia	5'- AYY-AAg-TCT-TTT-gAT-ggg-TC-3'	20	40	50.0	3507-3526	1058	1
	RT-FO3 1st RTb	5'-CTg-gAC-TgT-CAA-TgA-YAT-ACA-RA-3'	23	39.1	52.3	3302-3324	1102	1	
RT-b	RT-RO2	1 KID	5'-CCT-ggA-CTA-CAg-TCT-ACT-TgT-CC-3'	23	52.2	56.2	4382-4404	1102	
	RT-FI3	2 <sup>nd</sup> RTb	5'- gTC-AAT-gAY-ATA-CAR-AAR-TTA-gTR-gg-3'	26	34.6	51.8	3309-3334	096	
	RT-RI2	Z KID	5'-CAT-TgC-TCT-CCA-ATT-RCT-gTg-3'	21	45.2	53.1	4275-4295	986	

<sup>\*</sup> Reverse oligonucleotide primer sequences given in this table are the reverse-complement of the sequence present in the alignments and as they should be ordered for synthesis.



<sup>†</sup> Primer binding sites given on table are based on HXB2 reference sequence.



## RT-PCR components and conditions

Using Vivantis M-MuLV RT enzyme (Cat: ME2305) and Vivantis Taq DNA Pol (Cat: PL1202).

#### First strand synthesis (RT)

I II De Del Miles DJ memedia (III)	,	
	cf	1x
$dH_2O$		2.5 μL
10 μM Forward oligo	1.125 μM	2.3 μL
10 μM Reverse oligo	1.125 μM	2.3 μL
10 mM dNTPs 10 mM	250 μΜ	0.5 μL
RNA		10 μL
		vf: 17.6 ul

		•
RT Buffer	1x cf	2 μL
RT Enzyme 250 IU/μ1	5 IU/μL	0.4 μL
	_	vf: 20 μ1

Run RT-2 program in Axygen TC-1

	RT-1 pro	RT-1 program in Axygen TC-1					
	Total time: 6 min						
	95 ℃	95 °C 2 min					
•	4 °C	2 min	1 cycle				

RT-2 program in Axygen TC-1					
Total time: 1:12 hrs					
38 °C	60 min	1 cycle			
95 ℃	5 min				
4 °C	5 min				

## 1st Polymerase Chain Reaction (PCR) both fragments

	cf	1x
$dH_2O$	$\mathbf{C}f$	6.02
10x Buffer PCR	1x	1.25
MgCl <sub>2</sub> 50 mM	1.50 mM	0.38
dNTPs 10 mM	200 μΜ	0.25
Oligos 10 μM	400 nM	0.50
Taq (Vivantis) 5 UI/μL	0.04 UI/μL	0.10
DNA	-	4.00
		vf: 12.5 μl

Run 1 <sup>st</sup> PCR in Axygen cycler				
Total time: 1:30 hrs				
95 °C 2 min				
95 °C	30 sec			
55 <sup>a</sup> /54 <sup>b</sup> °C	45 sec	30 cycles		
72 °C	1 min			
72 °C	5 min			

# 2<sup>nd</sup> Polymerase Chain Reaction (PCR) both fragments

• •		
	cf	1x
$dH_2O$	$\mathbf{C}f$	9.02
10x Buffer PCR	1x	1.25
MgCl <sub>2</sub> 50 mM	1.50 mM	0.38
dNTPs 10 mM	200 μΜ	0.25
Oligos 10 μM	400 nM	0.50
Taq (Vivantis) 5 UI/μL	0.04 UI/μL	0.10
1 <sup>st</sup> PCR product	-	1.00
		vf: 12.5 ul

Run 2 <sup>nd</sup> PCR in Axygen cycler				
Total time: 1:30 hrs				
95 ℃				
95 ℃	30 sec			
51 <sup>a</sup> / 54 <sup>b</sup> °C	30 sec	30 cycles		
72 °C	1 min			
72 °C	5 min			





#### Notes

- 1. Clean workbench with 0.1% NaOCl 0.1% followed by 70% Ethanol before and after work.
- 2. Preparation of RT mastermix should only be performed in the RT-PCR room.
- 3. Preparation of PCR mastermix and addition of sample DNA should only be performed in the pre-PCR enclosure or area.
- 4. Addition of positive template DNA should be performed on instrument (post-PCR) area.
- 5. All mastermixes should be prepared on ice to prevent excess evaporation.
- 6. Vortex and spin all mastermixes before and after aliquoting to PCR tubes.

#### References

1. Swanson P, Devare SG, Hackett J Jr. Molecular characterization of 39 HIV isolates representing group M (subtypes A-G) and group O: sequence analysis of gag p24, pol integrase, and env gp41. AIDS Res Hum Retroviruses. 2003 Jul;19(7):625-9. PubMed PMID: 12921095.

## **Revision history**

- 1.0 Original document.
- 2.0 Changes to document format only.

